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<110> Stratagene

<120> HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR

<130> 25436/2152

<140> 10/035,091

<141> 2001-12-21

<160> 11

<170> PatentIn version 3.1

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<222> (2)..(3)

<223> Conserved domain, X at position 2 or 3 is any amino acid.

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Asp Xaa Xaa Ser Leu Tyr Pro

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<223> Conserved domain, X at position 2, 3, 4, or 7 is any amino acid.

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<222> (2)..(3)

<223> Conserved domain, X at position 2 or 3 is any amino acid.

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Thr Xaa Xaa Gly Arg

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<222> (2)..(2)

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Lys Xaa Tyr

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<210> 6

<211> 4

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Tyr Xaa Gly Gly

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<210> 7

<211> 6

<212> PRT

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Ser Tyr Thr Gly Gly Phe

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<212> DNA

<213> Artificial Sequence

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<213> Thermococcus sp. JDF-3

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Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile

35 40 45

Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys

50 55 60

Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val

65 70 75 80

Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile

85 90 95

Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr

100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro

115

120

125

Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr

130

135

140

Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile

145

150

155

160

Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile

165

170

175

Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys

180

185

190

Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr

195

200

205

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu

210

215

220

Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys

225 230 235 240

Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val

245 250 255

His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr

260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu

275 280 285

Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly

290 295 300

Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr

305 310 315 320

Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu

325 330 335

Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu

340

345

350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala

355

360

365

Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr

370

375

380

Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile

385

390

395

400

Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His

405

410

415

Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp

420

425

430

Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe

435

440

445

Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys

450

455

460

Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp

465

470

475

480

Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr

485

490

495

Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser

500

505

510

Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu

515

520

525

Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu

530

535

540

His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala

545

550

555

560

Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu

565

570

575

Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys

580

585

590

Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu

595

600

605

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala

610

615

620

Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val

625

630

635

640

Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro

645

650

655

Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp

660

665

670

Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala

675

680

685

Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu

690

695

700

Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe

705

710

715

720

Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln

725

730

735

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys

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Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp

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<210> 11

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<212> DNA

<213> Thermococcus sp. JDF-3

<400> 11

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